

CLAIMS

1. A detergent composition comprising an endo-glucanase, wherein the endo-glucanase is selected from one of:

- 5 (i) the endo-glucanase having the amino acid sequence of position 1 to position 773 of SEQ ID NO: 2;
- (ii) an endo-glucanase having a sequence of at least 90% identity to the amino acid sequence of position 1 to position 773 of SEQ ID NO:2; or a fragment thereof that has glucanase activity, when identity is determined by GAP provided in the GCG program package using a GAP creation penalty of 3.0 and GAP extension penalty of 0.1.

10 2. A detergent composition comprising an endo-glucanase, wherein the endo-glucanase is an anti-redeposition endo-glucanase as determined by the test for endo-glucanase activity together with the test for anti-redeposition effect.

- 15 3. A detergent composition comprising anionic tensides and a combination of an endo-glucanase as described in claims 1 or 2 and a fungal cellulase, wherein both enzymes are stable in the presence of anionic tensides.

20 4. The detergent composition of claim 3, wherein

- (a) the endo-glucanase is selected from one of:

- (i) the endo-glucanase having the amino acid sequence of position 1 to position 773 of SEQ ID NO: 2;
- (ii) an endo-glucanase having a sequence of at least 90% identity to the amino acid sequence of position 1 to position 773 of SEQ ID NO:2; or a fragment thereof that has glucanase activity, when identity is determined by GAP provided in the GCG program package using a GAP creation penalty of 3.0 and GAP extension penalty of 0.1;

- (b) the cellulase is selected from one of:

- 30 (i) the cellulase having the amino acid sequence of position 1 to position 299 of SEQ ID NO: 4 or
- (ii) a cellulase having a sequence of at least 70% identity to the amino acid sequence of position 1 to position 299 of SEQ ID NO:4, or a fragment thereof that has cellulase activity, when identity is determined by GAP provided in the GCG program package using a GAP creation penalty of 3.0 and GAP extension penalty of 0.1.

5. The detergent composition of claims 1 to 4, wherein the endo-glucanase is active at a pH at least in the range of 4-11, preferably 5.5-10.5.
6. The detergent composition of claims 3 to 5, wherein cellulase is derived from a strain of the genus *Thielavia*, preferably a strain of *Thielavia terrestris*, especially *Thielavia terrestris* NRRL 8126 and shown in SEQ ID NO: 4.
7. The composition of claims 1 to 6, wherein the composition further comprises one or more enzymes selected from the group consisting of proteases, cellulases, beta-glucanases, hemicellulases, lipases, peroxidases, laccases, alpha--amylases, glucoamylases, cutinases, pectinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, pectate lyases, xyloglucanases, xylanases, pectin acetyl esterases, polygalacturonases, rhamnogalacturonases, pectin lyases, other mannanases, pectin methylesterases, cellobiohydrolases, transglutaminases; or mixtures thereof.
- 15 8. The composition of claim 7, wherein the protease is derived from a strain of *Bacillus*, preferably where the protease is a subtilisin selected from the group of subtilisin Novo, subtilisin Carlsberg, subtilisin 309, subtilisin 147 and subtilisin 168.
- 20 9. The composition of claim 8, wherein the lipase is derived from a strain of the genus *Humicola*, preferably a strain of *Humicola lanuginose*, especially *Humicola lanuginose* DSM4109.
10. The composition of claim 9, wherein the alpha-amylase is derived from a strain of the genus *Bacillus*, preferably a strain of *Bacillus* sp., especially *Bacillus* sp. DSM 12649, NCIB 25 12512, or NCIB 12513.
11. The composition of claim 10, wherein the mannanase is derived from a strain of the genus *Bacillus*, preferably *Bacillus licheniformis*, especially *Bacillus licheniformis* sp. I633
- 30 12. The composition of claim 11, wherein the pectate lyase is derived from a strain of the genus *Bacillus*, preferably *Bacillus subtilis*, especially *Bacillus subtilis* DSM14218
13. The composition of claim 12, wherein the cellulase is derived from a strain of the genus *Humicola*, preferably *Humicola insolens*, especially *Humicola insolens* DSM 1800.
- 35 14. A detergent composition comprising an anti-redeposition endo-glucanase and a cellulase, characterised in that the enzyme detergency benefit from the enzyme combination is higher

than, preferably at least 5 units higher than the enzyme detergency benefit of the same detergent composition without the anti-redeposition glucanase (the enzyme detergency benefit being determined by the wash test method of Example 6) .

- 5 15. A detergent composition comprising an anti-redeposition endo-glucanase and an amylase, characterised in that the enzyme detergency benefit from the enzyme combination is higher than, preferably at least 5 units higher than the enzyme detergency benefit of the same detergent composition without the anti-redeposition glucanase (the enzyme detergency benefit being determined by the wash test method of Example 7) .

- 10 16. A detergent composition comprising an anti-redeposition endo-glucanase and a protease, characterised in that the enzyme detergency benefit from the enzyme combination is higher than, preferably at least 5 units higher than the enzyme detergency benefit of the same detergent composition without the anti-redeposition glucanase (the enzyme detergency benefit being determined by the wash test method of Example 8) .

- 15 17. A detergent composition comprising an anti-redeposition endo-glucanase and a hemi-cellulase, characterised in that the enzyme detergency benefit from the enzyme combination is higher than, preferably at least 5 units higher than the enzyme detergency benefit of the same detergent composition without the anti-redeposition glucanase (the enzyme detergency benefit being determined by the wash test method of Example 9) .

20 18. A detergent composition of Claim 17 wherein the hemi-cellulase is a mannanase.

- 25 19. A detergent composition comprising an anti-redeposition endo-glucanase and a lipase, characterised in that the enzyme detergency benefit from the enzyme combination is higher than, preferably at least 5 units higher than the enzyme detergency benefit of the same detergent composition without the anti-redeposition glucanase (the enzyme detergency benefit being determined by the wash test method of Example 11) .

- 30 20. A detergent composition comprising an anti-redeposition endo-glucanase and a pectinase or pectate lyase, characterised in that the enzyme detergency benefit from the enzyme combination is higher than, preferably at least 5 units higher than the enzyme detergency benefit of the same detergent composition without the anti-redeposition glucanase (the enzyme detergency benefit being determined by the wash test method of Example 10).

21. The detergent composition according to any of claims 14-20, wherein the endo-glucanase comprises the amino acid sequence of SEQ ID NO: 2, or an endo-glucanase having a sequence of at least 90% identity to the amino acid sequence of position 1 to position 773 of SEQ ID NO:2; or a fragment thereof that has endo-glucanase activity, when identity is determined by GAP provided in the GCG program package using a GAP creation penalty of 3.0 and GAP extension penalty of 0.1.
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22. A process for washing a fabric, comprising contacting a fabric with an aqueous solution of a composition of claims 1 to 21, optionally under agitation, for an effective period of time.
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23. The process of claim 22, wherein the period of time is between 2 minutes and 24 hours, preferably 10 minutes to 60 minutes.
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24. A process of claim 23, wherein the weight ratio of the endo-glucanase protein component to the total enzyme protein is less than 1:2.
25. A process for washing a hard surface, comprising contacting the surface with an aqueous solution of a composition of claims 1 to 21 for an effective period of time.
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26. The process of claim 22, wherein the period of time is between 1 minute and 1 hour, preferably 5 minutes to 30 minutes.
27. A process of anyone of claims 22 or 25, wherein the weight ratio of the endo-glucanase protein component to the total enzyme protein is less than 1:2.

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